

SEQUENCE LISTING

<110> University of Rochester

Chang, Chawnshang

<120> Non-androgen Dependent Roles for
Androgen Receptor and Non-androgen Related Inhibitors of
Androgen Receptor

<130> 21108.0037P1

<140> Unassigned

<141> 2004-12-13

<150> 60/529,011

<151> 2003-12-12

<160> 23

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 1

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1 5 10 15
Ala Ile Ser Ala Val Val Asp Asn Tyr Ile Arg Ser Arg Arg Asp Ile
20 25 30
Arg Ser Leu Pro Glu Asn Ile Gln Phe Asp Val Tyr Tyr Lys Leu Tyr
35 40 45
Gln Gln Gly Arg Leu Cys Gln Leu Gly Ser Glu Phe Cys Glu Leu Glu
50 55 60
Val Phe Ala Lys Val Leu Arg Ala Leu Asp Lys Arg His Leu Leu His
65 70 75 80
His Cys Phe Gln Ala Leu Met Asp His Gly Val Lys Val Ala Ser Val
85 90 95
Leu Ala Tyr Ser Phe Ser Arg Arg Cys Ser Tyr Ile Ala Glu Ser Asp
100 105 110
Ala Ala Val Lys Glu Lys Ala Ile Gln Val Gly Phe Val Leu Gly Gly
115 120 125
Phe Leu Ser Asp Ala Gly Trp Tyr Ser Asp Ala Glu Lys Val Phe Leu
130 135 140
Ser Cys Leu Gln Leu Cys Thr Leu His Asp Glu Met Leu His Trp Phe
145 ~ 150 155 160
Arg Ala Val Glu Cys Cys Val Arg Leu Leu His Val Arg Asn Gly Asn
165 170 175
Cys Lys Tyr His Leu Gly Glu Glu Thr Phe Lys Leu Ala Gln Thr Tyr
180 185 190
Met Asp Lys Leu Ser Lys His Gly Gln Gln Ala Asn Lys Ala Ala Leu
195 200 205
Tyr Gly Glu Leu Cys Ala Leu Leu Phe Ala Lys Ser His Tyr Asp Glu
210 215 220

Ala Tyr Lys Trp Cys Ile Glu Ala Met Lys Glu Ile Thr Ala Gly Leu
 225 230 235 240
 Pro Val Lys Val Val Val Asp Val Leu Arg Gln Ala Ser Lys Ala Cys
 245 250 255
 Val Val Lys Arg Glu Phe Lys Lys Ala Glu Gln Leu Ile Lys His Ala
 260 265 270
 Val Tyr Leu Ala Arg Asp His Phe Gly Ser Lys His Pro Lys Tyr Ser
 275 280 285
 Asp Thr Leu Leu Asp Tyr Gly Phe Tyr Leu Leu Asn Val Asp Asn Ile
 290 295 300
 Cys Gln Ser Val Ala Ile Tyr Gln Ala Ala Leu Asp Ile Arg Gln Ser
 305 310 315 320
 Val Phe Gly Gly Lys Asn Ile His Val Ala Thr Ala His Glu Asp Leu
 325 330 335
 Ala Tyr Ser Ser Tyr Val His Gln Tyr Ser Ser Gly Lys Phe Asp Asn
 340 345 350
 Ala Leu Phe His Ala Glu Arg Ala Ile Gly Ile Ile Thr His Ile Leu
 355 360 365
 Pro Glu Asp His Leu Leu Leu Ala Ser Ser Lys Arg Val Lys Ala Leu
 370 375 380
 Ile Leu Glu Glu Ile Ala Ile Asp Cys His Asn Lys Glu Thr Glu Gln
 385 390 395 400
 Arg Leu Leu Gln Glu Ala His Asp Leu His Leu Ser Ser Leu Gln Leu
 405 410 415
 Ala Lys Lys Ala Phe Gly Glu Phe Asn Val Gln Thr Ala Lys His Tyr
 420 425 430
 Gly Asn Leu Gly Arg Leu Tyr Gln Ser Met Arg Lys Phe Lys Glu Ala
 435 440 445
 Glu Glu Met His Ile Lys Ala Ile Gln Ile Lys Glu Gln Leu Leu Gly
 450 455 460
 Gln Glu Asp Tyr Glu Val Ala Leu Ser Val Gly His Leu Ala Ser Leu
 465 470 475 480
 Tyr Asn Tyr Asp Met Asn Gln Tyr Glu Asn Ala Glu Lys Leu Tyr Leu
 485 490 495
 Arg Ser Ile Ala Ile Gly Lys Lys Leu Phe Gly Glu Gly Tyr Ser Gly
 500 505 510
 Leu Glu Tyr Asp Tyr Arg Gly Leu Ile Lys Leu Tyr Asn Ser Ile Gly
 515 520 525
 Asn Tyr Glu Lys Val Phe Glu Tyr His Asn Val Leu Ser Asn Trp Asn
 530 535 540
 Arg Leu Arg Asp Arg Gln Tyr Ser Val Thr Asp Ala Leu Glu Asp Val
 545 550 555 560
 Ser Thr Ser Pro Gln Ser Thr Glu Glu Val Val Gln Ser Phe Leu Ile
 565 570 575
 Ser Gln Asn Val Glu Gly Pro Ser Cys
 580 585

<210> 2
 <211> 1758
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 2
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 gtcgtggaca actacatccg ctccccccga gacatccgct ctttgcggga gaacatccag 120
 ttgtatgtt actacaagct ttaccaacag ggacgcttat gtcaactggg cagtgaattt 180
 tgtgaattgg aagttttgc taaagtactg agagcttgg ataaaagaca tttgcttcatt 240

cattgttttc aggctttgat ggatcatggt gttaaagttg cttcagtctt ggctactca	300
ttcagtaggc ggtgctcta tatagcagaa tcagatgctg cagtaaagga aaaagccatt	360
cagggtggct ttgttttagg tggctttctt tcagatgcag gctggtagtg tgatgctgag	420
aaagttttc tgcctgcct tcagttgtgt actctacacg atgagatgct tcattggtt	480
cgtgcagtag aatgttgtgt gaggttgctt catgtgcgaa atggaaactg caaatatcat	540
ttgggtgaag aaacattaa attagctcg acatatatgg ataaactatc aaaacatggc	600
cagcaagcaa ataaagctgc actctatgga gaactgtgtg cactcctatt tgcaaaaagt	660
cactatgatg aggcatacaa atggtgcatc gaggcaatga aagaaattac agcaggctta	720
ccagtgaaag ttgtggtgga tgtcttaaga caagcttcta aggcttgtgt agtaaaacgt	780
gaatttaaga aggcaaca gttaaattaaa catgcagtgt atttggcacg ggatcattt	840
ggatccaaac acccaaaata ttctgataca ctgctagatt atgggttcta cttactcaat	900
gtagataata tctgtcagtc tggcaatt tatcaggcag cccttgacat tagacagtca	960
gtgtttggtg gcaaaaatat ccacgtca acagctcatg aagattggc ctactttct	1020
tatgtccacc agtatacgctc tggaaattt gacaatgcac tatttcatgc agaaagagct	1080
attggtatca ttacccacat cctacctgaa gatcatctc tttggcttc ttcaaagagg	1140
gtgaaagcac ttattttaga ggagattgca attgattgtc ataataagga aactgaacag	1200
aggctgcttc aagaagctca tgattgcac ctgtttcac tccaaactagc taaaaaagct	1260
tttgggaat ttaatgtaca gactgcaaaa cactatggaa accttggaaactttatcag	1320
tcaatgagaa aatttaagga agctgaagaa atgcacatca aagcaattca gattaaagaa	1380
caacttcttgc tcaagaaga ttatgaagta gcccatttcag tggacatct ggcttctt	1440
tataattatg acatgaatca gtatgaaaat gctgagaaac tttatttgcg atctatagca	1500
attgggaaga aacttttgg tgaggctac agtggactag aatatgatta tcgaggctc	1560
attaaacttt acaactccat tggaaattac gagaaagtgt ttgaatatca caatgttctg	1620
tctaactgga accgggtgcg agatcgcaaa tattcagtga cagatgctct tgaagatgtc	1680
agcaccagcc cccagtcac tgaagaagtg gtgcagtcct tcctgatttc tcagaatgtc	1740
gagggaccga gctgctga	1758

<210> 3

<211> 919

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 3

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1 5 10 15	
Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu	
20 25 30	
Val Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ala Ala	
35 40 45	
Pro Pro Gly Ala Ser Leu Leu Leu Gln Gln Gln Gln Gln Gln Gln	
50 55 60	
Gln Glu Thr	
65 70 75 80	
Ser Pro Arg Gln Gln Gln Gln Gln Gln Gly Glu Asp Gly Ser Pro Gln	
85 90 95	
Ala His Arg Arg Gly Pro Thr Gly Tyr Leu Val Leu Asp Glu Glu Gln	
100 105 110	
Gln Pro Ser Gln Pro Gln Ser Ala Leu Glu Cys His Pro Glu Arg Gly	
115 120 125	
Cys Val Pro Glu Pro Gly Ala Ala Val Ala Ala Ser Lys Gly Leu Pro	
130 135 140	
Gln Gln Leu Pro Ala Pro Pro Asp Glu Asp Asp Ser Ala Ala Pro Ser	
145 150 155 160	
Thr Leu Ser Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser Cys Ser	
165 170 175	
Ala Asp Leu Lys Asp Ile Leu Ser Glu Ala Ser Thr Met Gln Leu Leu	
180 185 190	

Gln Gln Gln Gln Glu Ala Val Ser Glu Gly Ser Ser Ser Gly Arg
 195 200 205
 Ala Arg Glu Ala Ser Gly Ala Pro Thr Ser Ser Lys Asp Asn Tyr Leu
 210 215 220
 Gly Gly Thr Ser Thr Ile Ser Asp Asn Ala Lys Glu Leu Cys Lys Ala
 225 230 235 240
 Val Ser Val Ser Met Gly Leu Gly Val Glu Ala Leu Glu His Leu Ser
 245 250 255
 Pro Gly Glu Gln Leu Arg Gly Asp Cys Met Tyr Ala Pro Leu Leu Gly
 260 265 270
 Val Pro Pro Ala Val Arg Pro Thr Pro Cys Ala Pro Leu Ala Glu Cys
 275 280 285
 Lys Gly Ser Leu Leu Asp Asp Ser Ala Gly Lys Ser Thr Glu Asp Thr
 290 295 300
 Ala Glu Tyr Ser Pro Phe Lys Gly Gly Tyr Thr Lys Gly Leu Glu Gly
 305 310 315 320
 Glu Ser Leu Gly Cys Ser Gly Ser Ala Ala Ala Gly Ser Ser Gly Thr
 325 330 335
 Leu Glu Leu Pro Ser Thr Leu Ser Leu Tyr Lys Ser Gly Ala Leu Asp
 340 345 350
 Glu Ala Ala Ala Tyr Gln Ser Arg Asp Tyr Tyr Asn Phe Pro Leu Ala
 355 360 365
 Leu Ala Gly Pro Pro Pro Pro Pro Pro His Pro His Ala Arg
 370 375 380
 Ile Lys Leu Glu Asn Pro Leu Asp Tyr Gly Ser Ala Trp Ala Ala Ala
 385 390 395 400
 Ala Ala Gln Cys Arg Tyr Gly Asp Leu Ala Ser Leu His Gly Ala Gly
 405 410 415
 Ala Ala Gly Pro Gly Ser Gly Ser Pro Ser Ala Ala Ala Ser Ser Ser
 420 425 430
 Trp His Thr Leu Phe Thr Ala Glu Glu Gly Gln Leu Tyr Gly Pro Cys
 435 440 445
 Gly
 450 455 460
 Gly Gly Gly Gly Gly Gly Glu Ala Gly Ala Val Ala Pro Tyr
 465 470 475 480
 Gly Tyr Thr Arg Pro Pro Gln Gly Leu Ala Gly Gln Glu Ser Asp Phe
 485 490 495
 Thr Ala Pro Asp Val Trp Tyr Pro Gly Gly Met Val Ser Arg Val Pro
 500 505 510
 Tyr Pro Ser Pro Thr Cys Val Lys Ser Glu Met Gly Pro Trp Met Asp
 515 520 525
 Ser Tyr Ser Gly Pro Tyr Gly Asp Met Arg Leu Glu Thr Ala Arg Asp
 530 535 540
 His Val Leu Pro Ile Asp Tyr Tyr Phe Pro Pro Gln Lys Thr Cys Leu
 545 550 555 560
 Ile Cys Gly Asp Glu Ala Ser Gly Cys His Tyr Gly Ala Leu Thr Cys
 565 570 575
 Gly Ser Cys Lys Val Phe Phe Lys Arg Ala Ala Glu Gly Lys Gln Lys
 580 585 590
 Tyr Leu Cys Ala Ser Arg Asn Asp Cys Thr Ile Asp Lys Phe Arg Arg
 595 600 605
 Lys Asn Cys Pro Ser Cys Arg Leu Arg Lys Cys Tyr Glu Ala Gly Met
 610 615 620
 Thr Leu Gly Ala Arg Lys Leu Lys Lys Leu Gly Asn Leu Lys Leu Gln
 625 630 635 640
 Glu Glu Gly Glu Ala Ser Ser Thr Thr Ser Pro Thr Glu Glu Thr Thr
 645 650 655
 Gln Lys Leu Thr Val Ser His Ile Glu Gly Tyr Glu Cys Gln Pro Ile
 660 665 670

Phe Leu Asn Val Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly
 675 680 685
 His Asp Asn Asn Gln Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu
 690 695 700
 Asn Glu Leu Gly Glu Arg Gln Leu Val His Val Val Lys Trp Ala Lys
 705 710 715 720
 Ala Leu Pro Gly Phe Arg Asn Leu His Val Asp Asp Gln Met Ala Val
 725 730 735
 Ile Gln Tyr Ser Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg
 740 745 750
 Ser Phe Thr Asn Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu
 755 760 765
 Val Phe Asn Glu Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys
 770 775 780
 Val Arg Met Arg His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr
 785 790 795 800
 Pro Gln Glu Phe Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile Ile
 805 810 815
 Pro Val Asp Gly Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met
 820 825 830
 Asn Tyr Ile Lys Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn
 835 840 845
 Pro Thr Ser Cys Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp
 850 855 860
 Ser Val Gln Pro Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu
 865 870 875 880
 Leu Ile Lys Ser His Met Val Ser Val Asp Phe Pro Glu Met Met Ala
 885 890 895
 Glu Ile Ile Ser Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys
 900 905 910
 Pro Ile Tyr Phe His Thr Gln
 915

<210> 4
<211> 4321
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 4
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agaggaggcg acagagggaa aaagggccga gctagccgct ccagtgtgt acaggagccg 120
aagggacgca ccacgcccagc cccagccccgg ctccagcgcac agccaacgccc tcttcagcg 180
cgccggcttc gaagccgccc cccggagctg ccctttcctc ttccgtgaag tttttaaaag 240
ctgctaaaga ctcggaggaa gcaaggaaag tgccctggtag gactgacggc tgcccttgc 300
ctccttcctc ccaccccgcc tccccccacc ctgccttccc cccctcccccc gtcttctctc 360
ccgcagctgc ctcagtcggc tacttcagc caacccccc caccaccctt ctccccaccc 420
gcccccccgcc ccccgctcggc ccagcgtgc cagcccgagt ttgcagagag gtaactccct 480
ttggctgcga gcggggcgagc tagctgcaca ttgcaaagaa ggctcttagg agccaggcga 540
ctggggagcg gcttcagcac tgcagccacg accccgcctgg tttagaattcc ggccggagaga 600
accctctgtt ttccccact ctctctccac ctcccttcgc cttcccccacc ccgagtgcgg 660
agcagagatc aaaagatgaa aaggcagtca ggtcttcagt agccaaaaaaa caaaacaaac 720
aaaaacaaaaa aagccgaaat aaaagaaaaaa gataataact cagttcttat ttgcacctac 780
ttcagtggac actgaatttg gaaggtggag gattttgttt ttttctttta agatctggc 840
atctttgaa tctacccttc aagtattaag agacagactg tgagcctagc agggcagatc 900
ttgtccaccg tgtgtcttct tctgcacgag actttgaggc tgtagcagcg ctttttgcgt 960
ggttgctccc gcaagttcc ttctctggag cttcccgccag gtggcagct agctgcagcg 1020
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ggaaagttagg	tggaagattc	agccaaagctc	aaggatggaa	gtgcagttag	ggctggaaag	1140
ggtctaccct	cggccgccgt	ccaagaccta	ccgaggagct	ttccagaatc	tgttccagag	1200
cgtgcgcgaa	gtgatccaga	acccgggccc	caggcaccca	gaggccgcga	gcgcagcacc	1260
tcccggcgcc	agtttgcgc	tgctgcagca	gcagcagcag	cagcagcagc	agcagcagca	1320
gcagcagcag	cagcagcagc	agcagcaaga	gactagcccc	aggcagcagc	agcagcagca	1380
gggtgaggat	ggttctccccc	aagcccatcg	tagaggcccc	acaggctacc	tggtcctgga	1440
tgaggaacag	caaccttcac	agccgcagtc	ggccctggag	tgccaccccg	agagaggttg	1500
cgtcccagag	cctggagccg	ccgtggccgc	cagcaagggg	ctgccgcagc	agctgccagc	1560
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acttttggga	gttccacccg	ctgtgcgtcc	cactccttgt	gccccattgg	ccgaatgcaa	1980
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gcccggaccg	ccgccccctc	cgccgcctcc	ccatccccac	gctcgcatca	agctggagaa	2280
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gaagctgaag	aaacttggta	atctgaaaact	acaggagaa	ggagaggctt	ccagcaccac	3060
cagccccact	gaggagacaa	cccagaagct	gacagtgtca	cacattgaag	gctatgaatg	3120
tcagcccatc	tttctgaatg	tcctggaa	cattgagcc	ggtgtatgt	gtgtggaca	3180
cgacaacaac	cagcccgact	cctttgcagc	cttgctctct	agcctcaatg	aactgggaga	3240
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cgtggacgac	cagatggctg	tcattcaga	ctcctggatg	gggctcatgg	tgttgccat	3360
gggctggcga	tccttcacca	atgtcaactc	caggatgctc	tacttcgccc	ctgatctggt	3420
tttcaatgag	taccgcac	acaagtcccg	gatgtacagc	cagtgtgtcc	gaatgaggca	3480
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tgcgagagag	ctgcacat	tcactttga	cctgctaatt	aagtacacaca	tggtgagcgt	3780
ggactttccg	gaaatgtgg	cagagatcat	ctctgtgca	gtgcccaga	tcctttctgg	3840
gaaagtcaag	cccatctatt	tccacaccca	gtgaagcatt	ggaaacccta	tttccccacc	3900
ccagctcatg	cccccttca	gatgtcttct	gcctgtata	actctgcact	actcctctgc	3960
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tggtgttgta	tgcctttaaa	tctgtatg	tcctcatatg	gcccagtgtc	aagttgtgt	4200
tgtttacagc	actactctgt	gccagccaca	caaacgttta	cttatcttat	gccacgggaa	4260
gttttagagag	ctaagattat	ctggggaaat	caaaaacaaaa	aacaagcaaa	caaaaaaaaaa	4320
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<210> 5
<211> 433
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 5

Met	Ser	Gly	Arg	Pro	Arg	Thr	Thr	Ser	Phe	Ala	Glu	Ser	Cys	Lys	Pro
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Val	Gln	Gln	Pro	Ser	Ala	Phe	Gly	Ser	Met	Lys	Val	Ser	Arg	Asp	Lys
									20	25					30
Asp	Gly	Ser	Lys	Val	Thr	Thr	Val	Val	Ala	Thr	Pro	Gly	Gln	Gly	Pro
									35	40					45
Asp	Arg	Pro	Gln	Glu	Val	Ser	Tyr	Thr	Asp	Thr	Lys	Val	Ile	Gly	Asn
									50	55					60
Gly	Ser	Phe	Gly	Val	Val	Tyr	Gln	Ala	Lys	Leu	Cys	Asp	Ser	Gly	Glu
									65	70					80
Leu	Val	Ala	Ile	Lys	Lys	Val	Leu	Gln	Asp	Lys	Arg	Phe	Lys	Asn	Arg
									85	90					95
Glu	Leu	Gln	Ile	Met	Arg	Lys	Leu	Asp	His	Cys	Asn	Ile	Val	Arg	Leu
									100	105					110
Arg	Tyr	Phe	Phe	Tyr	Ser	Ser	Gly	Glu	Lys	Lys	Asp	Glu	Val	Tyr	Leu
									115	120					125
Asn	Leu	Val	Leu	Asp	Tyr	Val	Pro	Glu	Thr	Val	Tyr	Arg	Val	Ala	Arg
									130	135					140
His	Tyr	Ser	Arg	Ala	Lys	Gln	Thr	Leu	Pro	Val	Ile	Tyr	Val	Lys	Leu
									145	150					160
Tyr	Met	Tyr	Gln	Leu	Phe	Arg	Ser	Leu	Ala	Tyr	Ile	His	Ser	Phe	Gly
									165	170					175
Ile	Cys	His	Arg	Asp	Ile	Lys	Pro	Gln	Asn	Leu	Leu	Leu	Asp	Pro	Asp
									180	185					190
Thr	Ala	Val	Leu	Lys	Leu	Cys	Asp	Phe	Gly	Ser	Ala	Lys	Gln	Leu	Val
									195	200					205
Arg	Gly	Glu	Pro	Asn	Val	Ser	Tyr	Ile	Cys	Ser	Arg	Tyr	Tyr	Arg	Ala
									210	215					220
Pro	Glu	Leu	Ile	Phe	Gly	Ala	Thr	Asp	Tyr	Thr	Ser	Ser	Ile	Asp	Val
									225	230					240
Trp	Ser	Ala	Gly	Cys	Val	Leu	Ala	Glu	Leu	Leu	Leu	Gly	Gln	Pro	Ile
									245	250					255
Phe	Pro	Gly	Asp	Ser	Gly	Val	Asp	Gln	Leu	Val	Glu	Ile	Ile	Lys	Val
									260	265					270
Leu	Gly	Thr	Pro	Thr	Arg	Glu	Gln	Ile	Arg	Glu	Met	Asn	Pro	Asn	Tyr
									275	280					285
Thr	Glu	Phe	Lys	Phe	Pro	Gln	Ile	Lys	Ala	His	Pro	Trp	Thr	Lys	Asp
									290	295					300
Ser	Ser	Gly	Thr	Gly	His	Phe	Thr	Ser	Gly	Val	Arg	Val	Phe	Arg	Pro
									305	310					320
Arg	Thr	Pro	Pro	Glu	Ala	Ile	Ala	Leu	Cys	Ser	Arg	Leu	Leu	Glu	Tyr
									325	330					335
Thr	Pro	Thr	Ala	Arg	Leu	Thr	Pro	Leu	Glu	Ala	Cys	Ala	His	Ser	Phe
									340	345					350
Phe	Asp	Glu	Leu	Arg	Asp	Pro	Asn	Val	Lys	Leu	Pro	Asn	Gly	Arg	Asp
									355	360					365
Thr	Pro	Ala	Leu	Phe	Asn	Phe	Thr	Thr	Gln	Glu	Leu	Ser	Ser	Asn	Pro
									370	375					380
Pro	Leu	Ala	Thr	Ile	Leu	Ile	Pro	Pro	His	Ala	Arg	Ile	Gln	Ala	Ala
									385	390					400
Ala	Ser	Thr	Pro	Thr	Asn	Ala	Thr	Ala	Ala	Ser	Asp	Ala	Asn	Thr	Gly
									405	410					415
Asp	Arg	Gly	Gln	Thr	Asn	Asn	Ala	Ala	Ser	Ala	Ser	Ala	Ser	Asn	Ser
									420	425					430
Thr															

<210> 6
<211> 1639
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 6

atcatctata	tgttaaatat	ccgtgccgat	ctgtcttgaa	ggagaaaatat	atcgcttggtt	60
ttgttttta	tagtatacaa	aaggagtgaa	aagccaagag	gacgaagtct	ttttcttttt	120
cttcgtggg	agaacttaat	gctgcattta	tcgttaacct	aacaccccaa	cataaagaca	180
aaaggaagaa	aaggaggaag	gaaggaaaag	gtgattcgcg	aagagagtga	tcatgtcagg	240
gcggcccaga	accacccct	ttgcggagag	ctgcaagccg	gtgcagcagc	cttcagctt	300
tggcagcatg	aaagtttagca	gagacaagga	cggcagcaag	gtgacaacag	tggtggcaac	360
tcctggcag	ggtccagaca	ggccacaaga	agtcagctat	acagacacta	aagtgattgg	420
aaatggatca	tttgggtgtgg	tatatcaagc	caaactttgt	gattcaggag	aactggtcgc	480
catcaagaaa	gtattgcagg	acaagagatt	taagaatcga	gagctccaga	tcatgagaaa	540
gctagatcac	tgtAACATAG	tccgattcgc	ttatTTCTTC	tactccagt	gtgagaagaa	600
agatgaggtc	tatCTTAATC	tggtgctgga	ctatgttccg	gaaacagtat	acagagttgc	660
cagacactat	agtcgagCCA	aacagacgct	ccctgtgatt	tatgtcaagt	tgtatATGTA	720
tcagctgttc	cgaagtttag	cctatATCCA	ttcCTTGGAA	atctGCCATC	gggatattaa	780
accgcagaac	ctcttgggtgg	atcctgatac	tgctgttatta	aaactctgt	actttggaaag	840
tgcaaAGCAG	ctggTCCGAG	gagaACCCAA	tgtttcgat	atctgttctc	ggtaCTATAAG	900
ggcaccagag	ttgatCTTTG	gagccactga	ttatacctct	agtatAGATG	tatggtctgc	960
tggctgtgt	ttggctgagc	tgttactagg	acaaccaata	tttccagggg	atagtgggt	1020
ggatcagttg	gtagaaataa	tcaaggtcct	gggaactcca	acaagggagc	aaatcagaga	1080
aatgaACCCA	aactacacag	aatttaaatt	ccctcaaatt	aaggcacatc	cttggactaa	1140
ggattcgtca	ggaacaggac	atttcacctc	aggagtgcgg	gtcttccgac	cccgaaCTCC	1200
accggaggca	attgcactgt	gtagccgtct	gctggagtat	acaccaactg	cccgactaac	1260
accactggaa	gcttgtgcac	attcattttt	tgatgaatta	cgggACCCAA	atgtcaaact	1320
accaaATGGG	cgagacacac	ctgcactctt	caacttcacc	actcaagaac	tgtcaagtaa	1380
tccacCTCTG	gctaccatcc	ttattcctcc	tcatgctcg	attcaagcag	ctgcttcaac	1440
ccccacAAAT	gccacAGCAG	cgtcagatgc	taatactgga	gaccgtggac	agaccaataa	1500
tgctgcttct	gcatcagctt	ccaaCTCCAC	ctgaacagtc	ccgagcagcc	agctgcacag	1560
aaaaaaACCAc	cagttacttg	agtgtcactc	agcaacactg	gtcacgttt	gaaagaatat	1620
aaaaaaaaaa	aaaaaaaaaa					1639

<210> 7
<211> 391
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 7

Met	Lys	Cys	Leu	Val	Thr	Gly	Gly	Asn	Val	Lys	Val	Leu	Gly	Lys	Ala
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Val	His	Ser	Leu	Ser	Arg	Ile	Gly	Asp	Glu	Leu	Tyr	Leu	Glu	Pro	Leu
									20					25	30
Glu	Asp	Gly	Leu	Ser	Leu	Arg	Thr	Val	Asn	Ser	Ser	Arg	Ser	Ala	Tyr
									35					40	45
Ala	Cys	Phe	Leu	Phe	Ala	Pro	Leu	Phe	Phe	Gln	Gln	Tyr	Gln	Ala	Ala
									50					55	60
Thr	Pro	Gly	Gln	Asp	Leu	Leu	Arg	Cys	Lys	Ile	Leu	Met	Lys	Ser	Phe
									65					70	75
															80

Leu Ser Val Phe Arg Ser Leu Ala Met Leu Glu Lys Thr Val Glu Lys
 85 90 95
 Cys Cys Ile Ser Leu Asn Gly Arg Ser Ser Arg Leu Val Val Gln Leu
 100 105 110
 His Cys Lys Phe Gly Val Arg Lys Thr His Asn Leu Ser Phe Gln Asp
 115 120 125
 Cys Glu Ser Leu Gln Ala Val Phe Asp Pro Ala Ser Cys Pro His Met
 130 135 140
 Leu Arg Ala Pro Ala Arg Val Leu Gly Glu Ala Val Leu Pro Phe Ser
 145 150 155 160
 Pro Ala Leu Ala Glu Val Thr Leu Gly Ile Gly Arg Gly Arg Arg Val
 165 170 175
 Ile Leu Arg Ser Tyr His Glu Glu Ala Asp Ser Thr Ala Lys Ala
 180 185 190
 Met Val Thr Glu Met Cys Leu Gly Glu Glu Asp Phe Gln Gln Leu Gln
 195 200 205
 Ala Gln Glu Gly Val Ala Ile Thr Phe Cys Leu Lys Glu Phe Arg Gly
 210 215 220
 Leu Leu Ser Phe Ala Glu Ser Ala Asn Leu Asn Leu Ser Ile His Phe
 225 230 235 240
 Asp Ala Pro Gly Arg Pro Ala Ile Phe Thr Ile Lys Asp Ser Leu Leu
 245 250 255
 Asp Gly His Phe Val Leu Ala Thr Leu Ser Asp Thr Asp Ser His Ser
 260 265 270
 Gln Asp Leu Gly Ser Pro Glu Arg His Gln Pro Val Pro Gln Leu Gln
 275 280 285
 Ala His Ser Thr Pro His Pro Asp Asp Phe Ala Asn Asp Asp Ile Asp
 290 295 300
 Ser Tyr Met Ile Ala Met Glu Thr Thr Ile Gly Asn Glu Gly Ser Arg
 305 310 315 320
 Val Leu Pro Ser Ile Ser Leu Ser Pro Gly Pro Gln Pro Pro Lys Ser
 325 330 335
 Pro Gly Pro His Ser Glu Glu Glu Asp Glu Ala Glu Pro Ser Thr Val
 340 345 350
 Pro Gly Thr Pro Pro Pro Lys Lys Phe Arg Ser Leu Phe Phe Gly Ser
 355 360 365
 Ile Leu Ala Pro Val Arg Ser Pro Gln Gly Pro Ser Pro Val Leu Ala
 370 375 380
 Glu Asp Ser Glu Gly Glu Gly
 385 390

<210> 8
 <211> 2102
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 8
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 ggagcgctgg ggcagcatga agtgccttgtt cacggggggc aacgtgaagg tgctcgccaa 120
 ggccgtccac tccctgtccc gcatggggga cgagctctac ctggAACCCt tggaggacgg 180
 gctctccctc cggacggta actccctcccg ctctgcctat gcctgctttc tctttgcccc 240
 gctcttcttc cagcaatacc aggccagccac ccctggtcag gacctgctgc gctgtaagat 300
 cctgatgaag tcttcctgt ctgtcttccg ctcactggcg atgctggaga agacggtgaa 360
 aaaatgctgc atctccctga atggccggag cagccgcctg gtggtccagc tgcattgcaa 420
 ttccgggtg cggaaagactc acaacctgtc cttccaggac tgtgagtccc tgcaggccgt 480
 cttcgaccga gcctcggtcc cccacatgtc ccgcggccca gcacgggttc tgggggaggc 540
 tgttctgccc ttctctcctg cactggctga agtgcacgctg ggcattggcc gtggccgcag 600

ggtcatcctg	cgcagctacc	acgaggagga	ggcagacagc	actgccaaag	ccatggtac	660
tgagatgtgc	cttggagagg	aggatttcca	gcagctgcag	gcccaggaag	gggtggccat	720
cactttctgc	ctcaaggaat	tccggggct	cctgagctt	gcagagttag	caaactttag	780
tcttagcatt	cattttgatg	ctccaggcag	gcccgcac	ttcaccatca	aggactctt	840
gctggacggc	cactttgtct	tggccacact	ctcagacacc	gactcgact	cccaggac	900
gggctcccc	gagcgtcacc	agccagtgcc	tcagctccag	gctcacagca	caccccaccc	960
ggacgactt	gccaatgacg	acattgactc	ttacatgatc	gccatggaaa	ccactatagg	1020
caatgagggc	tcgcgggtgc	tgccctccat	ttcccttca	cctggccccc	agccccccaa	1080
gagccccgt	ccccactccg	aggaggaaga	tgaggctgag	cccagtacag	tgcctggac	1140
tcccccaccc	aagaagttcc	gctcactgtt	cttcggctcc	atcctggccc	ctgtacgctc	1200
cccccaggc	cccagccctg	tgctggcgg	agacagttag	ggtgaaggct	gaaccaagaa	1260
cctgaaggct	gtacccagag	gccttggact	agacgaagcc	ccagccagtg	gcagaactgg	1320
gtctctcagc	cctggggatc	agaaaggtgg	gcttgctgga	gctgagctgt	ttcactgcct	1380
ctcgcaggcc	ccagctggct	gtcactgtaa	agctgtccca	cagcggtcgg	gcctggcccg	1440
ttatctcccc	acaacccca	gccaatcagg	actttccaga	cttggccctg	aactactgac	1500
gttcctacct	cttatttctc	attgagcctc	aggctatact	ccagctggcc	aaggctggaa	1560
acctgtctcc	ctcaggctca	ccttcctaag	gaaaatgtca	tagtaggtgc	tgctggccccc	1620
tggtgatcca	gcttctctgc	caatcatgac	ctgttccttc	ctgaagtcct	gggcatgcat	1680
ctgggacccc	cgtggagctg	acaagtttc	cttgcttcc	tgatacttt	tggcgctgac	1740
ttggaattct	aagagcctt	gacccgagt	tgtggctagg	gttgcctgg	ctggggcccg	1800
gtgccgagac	tcccaagcgg	ctctgtgcag	aagagctgcc	aggcagtgtc	ttagatgtga	1860
gacggaggcc	atggcgagaa	tccagcttt	accttattc	aagagaccag	atgggttgcc	1920
ccaggatccg	gctgccagcc	ctgaggccaa	gcacggctgg	agacccacga	cctggcctgc	1980
cgttgcctg	agctgcagcc	tcggccccag	gatcctgctc	acagtcaccg	caggtgcagg	2040
caggaagcag	ccctggggga	ctggacgctg	ctattgattc	attaaaaaaa	gaaaagaaaa	2100
at						2102

<210> 9
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 9
gggccccctgg atggatagct ac 22

<210> 10
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 10
gtagctatcc atccaggggc c 21

<210> 11
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 11

gggccccctgg atggatagct acctcgaggt agctatccat ccaggggcc

49

<210> 12
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 12
tttttgggcc cctggatgga tagctacctc gaggttagcta tccatccagg ggcc

54

<210> 13
<211> 483
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 13
Met Ala Thr Ile Glu Glu Ile Ala His Gln Ile Ile Glu Gln Gln Met
1 5 10 15
Gly Glu Ile Val Thr Glu Gln Gln Thr Gly Gln Lys Ile Gln Ile Val
20 25 30
Thr Ala Leu Asp His Asn Thr Gln Gly Lys Gln Phe Ile Leu Thr Asn
35 40 45
His Asp Gly Ser Thr Pro Ser Lys Val Ile Leu Ala Arg Gln Asp Ser
50 55 60
Thr Pro Gly Lys Val Phe Leu Thr Thr Pro Asp Ala Ala Gly Val Asn
65 70 75 80
Gln Leu Phe Phe Thr Thr Pro Asp Leu Ser Ala Gln His Leu Gln Leu
85 90 95
Leu Thr Asp Asn Ser Pro Asp Gln Gly Pro Asn Lys Val Phe Asp Leu
100 105 110
Cys Val Val Cys Gly Asp Lys Ala Ser Gly Arg His Tyr Gly Ala Val
115 120 125
Thr Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Ser Ile Arg Lys Asn
130 135 140
Leu Val Tyr Ser Cys Arg Gly Ser Lys Asp Cys Ile Ile Asn Lys His
145 150 155 160
His Arg Asn Arg Cys Gln Tyr Cys Arg Leu Gln Arg Cys Ile Ala Phe
165 170 175
Gly Met Lys Gln Asp Ser Val Gln Cys Glu Arg Lys Pro Ile Glu Val
180 185 190
Ser Arg Glu Lys Ser Ser Asn Cys Ala Ala Ser Thr Glu Lys Ile Tyr
195 200 205
Ile Arg Lys Asp Leu Arg Ser Pro Leu Thr Ala Thr Pro Thr Phe Val
210 215 220
Thr Asp Ser Glu Ser Thr Arg Ser Thr Gly Leu Leu Asp Ser Gly Met
225 230 235 240
Phe Met Asn Ile His Pro Ser Gly Val Lys Thr Glu Ser Ala Val Leu
245 250 255
Met Thr Ser Asp Lys Ala Glu Ser Cys Gln Gly Asp Leu Ser Thr Leu
260 265 270
Ala Asn Val Val Thr Ser Leu Ala Asn Leu Gly Lys Thr Lys Asp Leu
275 280 285

Ser Gln Asn Ser Asn Glu Met Ser Met Ile Glu Ser Leu Ser Asn Asp
 290 295 300
 Asp Thr Ser Leu Cys Glu Phe Gln Glu Met Gln Thr Asn Gly Asp Val
 305 310 315 320
 Ser Arg Ala Phe Asp Thr Leu Ala Lys Ala Leu Asn Pro Gly Glu Ser
 325 330 335
 Thr Ala Cys Gln Ser Ser Val Ala Gly Met Glu Gly Ser Val His Leu
 340 345 350
 Ile Thr Gly Asp Ser Ser Ile Asn Tyr Thr Glu Lys Glu Gly Pro Leu
 355 360 365
 Leu Ser Asp Ser His Val Ala Phe Arg Leu Thr Met Pro Ser Pro Met
 370 375 380
 Pro Glu Tyr Leu Asn Val His Tyr Ile Gly Glu Ser Ala Ser Arg Leu
 385 390 395 400
 Leu Phe Leu Ser Met His Trp Ala Leu Ser Ile Pro Ser Phe Gln Ala
 405 410 415
 Leu Gly Gln Glu Asn Ser Ile Ser Leu Val Lys Ala Tyr Trp Asn Glu
 420 425 430
 Leu Phe Thr Leu Gly Leu Ala Gln Cys Trp Gln Val Met Asn Val Ala
 435 440 445
 Thr Ile Leu Ala Thr Phe Val Asn Cys Leu His Asn Ser Leu Gln Gln
 450 455 460
 Asp Ala Lys Val Ile Ala Ala Leu Ile His Phe Thr Arg Arg Ala Ile
 465 470 475 480
 Thr Asp Leu

<210> 14
 <211> 596
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 14
 Met Thr Ser Pro Ser Pro Arg Ile Gln Ile Ile Ser Thr Asp Ser Ala
 1 5 10 15
 Val Ala Ser Pro Gln Arg Ile Gln Ile Val Thr Asp Gln Gln Thr Gly
 20 25 30
 Gln Lys Ile Gln Ile Val Thr Ala Val Asp Ala Ser Gly Ser Pro Lys
 35 40 45
 Gln Gln Phe Ile Leu Thr Ser Pro Asp Gly Ala Gly Thr Gly Lys Val
 50 55 60
 Ile Leu Ala Ser Pro Glu Thr Ser Ser Ala Lys Gln Leu Ile Phe Thr
 65 70 75 80
 Thr Ser Asp Asn Leu Val Pro Gly Arg Ile Gln Ile Val Thr Asp Ser
 85 90 95
 Ala Ser Val Glu Arg Leu Leu Gly Lys Thr Asp Val Gln Arg Pro Gln
 100 105 110
 Val Val Glu Tyr Cys Val Val Cys Gly Asp Lys Ala Ser Gly Arg His
 115 120 125
 Tyr Gly Ala Val Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Ser
 130 135 140
 Val Arg Lys Asn Leu Thr Tyr Ser Cys Arg Ser Asn Gln Asp Cys Ile
 145 150 155 160
 Ile Asn Lys His His Arg Asn Arg Cys Gln Phe Cys Arg Leu Lys Lys
 165 170 175
 Cys Leu Glu Met Gly Met Lys Met Glu Ser Val Gln Ser Glu Arg Lys
 180 185 190

Pro Phe Asp Val Gln Arg Glu Lys Pro Ser Asn Cys Ala Ala Ser Thr
 195 200 205
 Glu Lys Ile Tyr Ile Arg Lys Asp Leu Arg Ser Pro Leu Ile Ala Thr
 210 215 220
 Pro Thr Phe Val Ala Asp Lys Asp Gly Ala Arg Gln Thr Gly Leu Leu
 225 230 235 240
 Asp Pro Gly Met Leu Val Asn Ile Gln Gln Pro Leu Ile Arg Glu Asp
 245 250 255
 Gly Thr Val Leu Leu Ala Thr Asp Ser Lys Ala Glu Thr Ser Gln Gly
 260 265 270
 Ala Leu Gly Thr Leu Ala Asn Val Val Thr Ser Leu Ala Asn Leu Ser
 275 280 285
 Glu Ser Leu Asn Asn Gly Asp Thr Ser Glu Ile Gln Pro Glu Asp Gln
 290 295 300
 Ser Ala Ser Glu Ile Thr Arg Ala Phe Asp Thr Leu Ala Lys Ala Leu
 305 310 315 320
 Asn Thr Thr Asp Ser Ser Ser Pro Ser Leu Ala Asp Gly Ile Asp
 325 330 335
 Thr Ser Gly Gly Ser Ile His Val Ile Ser Arg Asp Gln Ser Thr
 340 345 350
 Pro Ile Ile Glu Val Glu Gly Pro Leu Leu Ser Asp Thr His Val Thr
 355 360 365
 Phe Lys Leu Thr Met Pro Ser Pro Met Pro Glu Tyr Leu Asn Val His
 370 375 380
 Tyr Ile Cys Glu Ser Ala Ser Arg Leu Leu Phe Leu Ser Met His Trp
 385 390 395 400
 Ala Arg Ser Ile Pro Ala Phe Gln Ala Leu Gly Gln Asp Cys Asn Thr
 405 410 415
 Ser Leu Val Arg Ala Cys Trp Asn Glu Leu Phe Thr Leu Gly Leu Ala
 420 425 430
 Gln Cys Ala Gln Val Met Ser Leu Ser Thr Ile Leu Ala Ala Ile Val
 435 440 445
 Asn His Leu Gln Asn Ser Ile Gln Glu Asp Lys Leu Ser Gly Asp Arg
 450 455 460
 Ile Lys Gln Val Met Glu His Ile Trp Lys Leu Gln Glu Phe Cys Asn
 465 470 475 480
 Ser Met Ala Lys Leu Asp Ile Asp Gly Tyr Glu Tyr Ala Tyr Leu Lys
 485 490 495
 Ala Ile Val Leu Phe Ser Pro Asp His Pro Gly Leu Thr Ser Thr Ser
 500 505 510
 Gln Ile Glu Lys Phe Gln Glu Lys Ala Gln Met Glu Leu Gln Asp Tyr
 515 520 525
 Val Gln Lys Thr Tyr Ser Glu Asp Thr Tyr Arg Leu Ala Arg Ile Leu
 530 535 540
 Val Arg Leu Pro Ala Leu Arg Leu Met Ser Ser Asn Ile Thr Glu Glu
 545 550 555 560
 Leu Phe Phe Thr Gly Leu Ile Gly Asn Val Ser Ile Asp Ser Ile Ile
 565 570 575
 Pro Tyr Ile Leu Lys Met Glu Thr Ala Glu Tyr Asn Gly Gln Ile Thr
 580 585 590
 Gly Ala Ser Leu
 595

<210> 15
 <211> 2029
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 15

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tggcagccgc gggactgtcg	cgtcgccgc cgacgcggag tcagcagggg	cgaaaagcgg	120
tagatcatgg caaccataga	agaaattgca catcaaatta ttgaacaaca	gatggagag	180
attgttacag agcagcaaac	tggcagaaa atccagatt tgacagcact	tgatcataat	240
acccaaggca agcagttcat	tctgacaaat cacgacggct ctactccaag	caaagtcat	300
ctggccaggc aagattccac	tccggaaaaa gtttcctta caactccaga	tgcagcaggt	360
gtcaaccagt tatttttac	cactcctgat ctgtctgcac aacacctgca	gctcctaaca	420
gataattctc cagaccaagg	accaaataag gttttgatc tttcgtagt	atgtggagac	480
aaagcatcag gacgtcatta	tggagcagta acttgtgaag gctgcaaagg	atttttaaa	540
agaagcatcc gaaaaaattt	agtatattca tgtcgaggat caaaggattt	tattattaat	600
aagcaccacc gaaaccgctg	tcaataactgc aggttacaga gatgtattgc	gtttggatg	660
aagcaagact ctgtccaatg	tgaaagaaaaa cccattgaag tatcacgaga	aaaatctcc	720
aactgtgccg cttcaacaga	aaaaatctat atccgaaagg accttcgtag	cccattaact	780
gcaactccaa cttttgtAAC	agatagtgaa agtacaaggt caacaggact	gttagattca	840
ggaatgtca tgaatattca	tccatctgga gtaaaaactg agtcagctgt	gctgatgaca	900
tcagataagg ctgaatcatg	tcagggagat ttaagtacat tggccaatgt	ggttacatca	960
ttagcgaatc ttggaaaaac	taaagatctt tctcaaaata gtaatgaaat	gtctatgatt	1020
gaaagcttaa gcaatgatga	tacctctttg tgtgaatttc aagaaatgca	gaccaacgg	1080
gatgttcaa gggcatttga	cactcttgca aaagcattga atcctggaga	gagcacagcc	1140
tgccagagct cagtagcggt	catggaagga agtgtacacc taatcactgg	agattcaagc	1200
ataaaattaca ccgaaaaaga	ggggccactt ctcagcgatt cacatgtgc	tttcaggctc	1260
accatgcctt ctcctatgcc	tgagtacctg aatgtgcact acattggga	gtctgcctcc	1320
agactgctgt tcttatcaat	gcactggca ctttcgattt cttctttcca	ggctctaggg	1380
caagaaaaaca gcatatcact	ggtgaaagct tactggaatg aacttttac	tcttggtctt	1440
gcccagtgct ggcaagtgat	gaatgttagca actatattag caacattgt	caattgtctt	1500
cacaatagtc ttcaacaaga	tgccaaggta attgcagccc tcattcattt	cacaagacga	1560
gcaatcactg atttataat	gcttaactat agaatggctt atgactaccc	aaaacagtgc	1620
cccatcaaca aatggggaaa	attgccttt gagctcagga ataatttata	aattggggac	1680
taccttttag ttcttttagca	tattcttattt cttattgttt tatataattt	ttaaatcatt	1740
tgcttcctcc ttatgtttaa	cagcagaggg gtaatcacct taaaatgtca	tcaaaaatag	1800
atctactaga aggtagcatc	acattccat cttacttatg gactcctacc	cctgggtcat	1860
gtcttatatg cctgtatgg	ttataaagcc taccttcagg aaagctatgg	ttgactaatt	1920
actaatggat gggtttaaa	catgtccctc tacaataat taaaatctt	caatgttga	1980
atataatgtg gaggtgttta	cctgagggcc tctctatctc cccgaattc		2029

<210> 16

<211> 6450

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 16

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gggagcccgag gagctggcg	agggcggtcg tcctggagc tgacttgct	ccgtcggtc	180
gccggcttca ccggaccgca	ggctcccggt gcagggccgg ggccagagct	cgcgtgtcg	240
cgggacatgc gctgcgtcgc	ctctaaccctc gggctgtgct cttttccag	gtggcccgcc	300
gttttctgag cttctgtccc	tgcggggaca cggctgcac cctgcccgc	gccacggacc	360
atgaccatga ccctccacac	caaagcatct gggatggccc tactgcata	gatccaagg	420
aacgagctgg agccctgaa	ccgtccgcag ctcaagatcc ccctggagcg	gcccctggc	480
gaggtgtacc tggacagcg	caagccgcgc gtgtacaact accccgaggg	cgccgcctac	540
gagttcaacg ccgcggccgc	cgccaaacgcg caggtctacg gtcagaccgg	cctccctac	600
ggcccccgggt ctgaggctgc	ggcggtcggc tccaaacggcc tgggggttt	ccccccactc	660
aacagcgtgt ctccgagccc	gctgtatgcta ctgcacccgc cgccgcagct	gtcgcccttc	720
ctgcagcccc acggccagca	ggtgcctac tacctggaga acgagcccag	cgctacacg	780
gtgcgcgagg ccggccgcgc	ggcattctac aggccaaatt cagataatcg	acgcccagggt	840

ggcagagaaa	gattggccag	taccaatgac	aaggaaagta	tggctatgga	atctgccaa	900
gagactcgct	actgtcagt	gtgcaatgac	tatgcttcag	gctaccatta	tggagtctgg	960
tcctgtgagg	gctgcaaggc	cttcttcaag	agaagtattc	aaggacataa	cgactatatg	1020
tgtccagcca	ccaaccagtg	caccattgat	aaaaacagga	ggaagagctg	ccaggcctgc	1080
cggctccgca	aatgctacga	agtggaaatg	atgaaaggtg	ggatacgaaa	agaccgaaga	1140
ggagggagaa	tgttcaaaca	caagcgccag	agagatgatg	gggagggcag	gggtgaagtg	1200
gggtctgctg	gagacatgag	agctgccaac	ctttggccaa	gcccgcctat	gatcaaacgc	1260
tctaagaaga	acagcctggc	cttgcctctg	acggccgacc	agatggtcag	tgccttgg	1320
gatgctgagc	ccccatact	ctattccgag	tatgatccta	ccagaccctt	cagtgaagct	1380
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 17
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<210> 18
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 18
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<210> 19

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
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synthetic construct

<400> 19
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<210> 20
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<212> DNA
<213> Artificial Sequence

<220>
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synthetic construct

<400> 20
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<210> 21
<211> 920
<212> PRT
<213> Artificial Sequence

<220>
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synthetic construct

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Val Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ala Ala
35 40 45
Pro Pro Gly Ala Ser Leu Leu Leu Gln Gln Gln Gln Gln Gln Gln
50 55 60
Gln
65 70 75 80
Glu Thr Ser Pro Arg Gln Gln Gln Gln Gln Gly Glu Asp Gly Ser
85 90 95
Pro Gln Ala His Arg Arg Gly Pro Thr Gly Tyr Leu Val Leu Asp Glu
100 105 110
Glu Gln Gln Pro Ser Gln Pro Gln Ser Ala Leu Glu Cys His Pro Glu
115 120 125
Arg Gly Cys Val Pro Glu Pro Gly Ala Ala Val Ala Ala Ser Lys Gly
130 135 140
Leu Pro Gln Gln Leu Pro Ala Pro Pro Asp Glu Asp Asp Ser Ala Ala
145 150 155 160
Pro Ser Thr Leu Ser Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser
165 170 175
Cys Ser Ala Asp Leu Lys Asp Ile Leu Ser Glu Ala Ser Thr Met Gln
180 185 190
Leu Leu Gln Gln Gln Gln Glu Ala Val Ser Glu Gly Ser Ser Ser
195 200 205
Gly Arg Ala Arg Glu Ala Ser Gly Ala Pro Thr Ser Ser Lys Asp Asn
210 215 220

Tyr Leu Gly Gly Thr Ser Thr Ile Ser Asp Asn Ala Lys Glu Leu Cys
 225 230 235 240
 Lys Ala Val Ser Val Ser Met Gly Leu Gly Val Glu Ala Leu Glu His
 245 250 255
 Leu Ser Pro Gly Glu Gln Leu Arg Gly Asp Cys Met Tyr Ala Pro Leu
 260 265 270
 Leu Gly Val Pro Pro Ala Val Arg Pro Thr Pro Cys Ala Pro Leu Ala
 275 280 285
 Glu Cys Lys Gly Ser Leu Leu Asp Asp Ser Ala Gly Lys Ser Thr Glu
 290 295 300
 Asp Thr Ala Glu Tyr Ser Pro Phe Lys Gly Gly Tyr Thr Lys Gly Leu
 305 310 315 320
 Glu Gly Glu Ser Leu Gly Cys Ser Gly Ser Ala Ala Ala Gly Ser Ser
 325 330 335
 Gly Thr Leu Glu Leu Pro Ser Thr Leu Ser Leu Tyr Lys Ser Gly Ala
 340 345 350
 Leu Asp Glu Ala Ala Ala Tyr Gln Ser Arg Asp Tyr Tyr Asn Phe Pro
 355 360 365
 Leu Ala Leu Ala Gly Pro Pro Pro Pro Pro Pro His Pro His
 370 375 380
 Ala Arg Ile Lys Leu Glu Asn Pro Leu Asp Tyr Gly Ser Ala Trp Ala
 385 390 395 400
 Ala Ala Ala Ala Gln Cys Arg Tyr Gly Asp Leu Ala Ser Leu His Gly
 405 410 415
 Ala Gly Ala Ala Gly Pro Gly Ser Gly Ser Pro Ser Ala Ala Ser
 420 425 430
 Ser Ser Trp His Thr Leu Phe Thr Ala Glu Glu Gly Gln Leu Tyr Gly
 435 440 445
 Pro Cys Gly
 450 455 460
 Gly Gly Gly Gly Gly Gly Gly Glu Ala Gly Ala Val Ala Pro
 465 470 475 480
 Tyr Gly Tyr Thr Arg Pro Pro Gln Gly Leu Ala Gly Gln Glu Ser Asp
 485 490 495
 Phe Thr Ala Pro Asp Val Trp Tyr Pro Gly Gly Met Val Ser Arg Val
 500 505 510
 Pro Tyr Pro Ser Pro Thr Cys Val Lys Ser Glu Met Gly Pro Trp Met
 515 520 525
 Asp Ser Tyr Ser Gly Pro Tyr Gly Asp Met Arg Leu Glu Thr Ala Arg
 530 535 540
 Asp His Val Leu Pro Ile Asp Tyr Tyr Phe Pro Pro Gln Lys Thr Cys
 545 550 555 560
 Leu Ile Cys Gly Asp Glu Ala Ser Gly Cys His Tyr Gly Ala Leu Thr
 565 570 575
 Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala Ala Glu Gly Lys Gln
 580 585 590
 Lys Tyr Leu Cys Ala Ser Arg Asn Asp Cys Thr Ile Asp Lys Phe His
 595 600 605
 Arg Lys Asn Cys Pro Ser Cys Arg Leu Arg Lys Cys Tyr Glu Ala Gly
 610 615 620
 Met Thr Leu Gly Ala Arg Lys Leu Lys Lys Leu Gly Asn Leu Lys Leu
 625 630 635 640
 Gln Glu Glu Gly Glu Ala Ser Ser Thr Thr Ser Pro Thr Glu Glu Thr
 645 650 655
 Thr Gln Lys Leu Thr Val Ser His Ile Glu Gly Tyr Glu Cys Gln Pro
 660 665 670
 Ile Phe Leu Asn Val Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala
 675 680 685
 Gly His Asp Asn Asn Gln Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser
 690 695 700

Leu Asn Glu Leu Gly Glu Arg Gln Leu Val His Val Val Lys Trp Ala
 705 710 715 720
 Lys Ala Leu Pro Gly Phe Arg Asn Leu His Val Asp Asp Gln Met Ala
 725 730 735
 Val Ile Gln Tyr Ser Trp Met Gly Leu Met Val Phe Ala Met Gly Trp
 740 745 750
 Arg Ser Phe Thr Asn Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp
 755 760 765
 Leu Val Phe Asn Glu Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln
 770 775 780
 Cys Val Arg Met Arg His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile
 785 790 795 800
 Thr Pro Gln Glu Phe Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile
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 Ile Pro Val Asp Gly Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg
 820 825 830
 Met Asn Tyr Ile Lys Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys
 835 840 845
 Asn Pro Thr Ser Cys Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu
 850 855 860
 Asp Ser Val Gln Pro Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp
 865 870 875 880
 Leu Leu Ile Lys Ser His Met Val Ser Val Asp Phe Pro Glu Met Met
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 Lys Pro Ile Tyr Phe His Thr Gln
 915 920

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<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 22

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<210> 23

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 23

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Pro Thr Met